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; SEQUENCE DESCRIPTION: SEQ ID NO: 6348:
US-09-107-532A-6348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6348, Ap
Sequence 5060, Ap
Sequence 31996, A
                                                                                January 30, 2004, 15:23:07; Search time 21 Seconds (without alignments) 1124.260 Million cell updates/sec
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Sequence 2, Appli
Sequence 5311, Ap
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1 MDQNSYRRRSSPIRTTTGGS......GTLVPHVRHCEDISWGLKLV 558
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Sequence 16
Sequence 2
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Sequence 6
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Sequence 2
Sequence 3
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-001C-5060
US-09-252-991A-31996
US-09-186-276B-58
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US-09-186-276B-58
US-09-489-847-352
US-09-222-617A-6
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
US-08-222-617A-2
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Sequence 7, Appli Sequence 7, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli		h SEQUENCES RELATING TO	AGNOSTICS		·		
584 1 US-08-179-738-7 584 2 US-08-628-145-7 591 1 US-08-628-145-7 591 2 US-08-628-145-5 596 1 US-08-628-145-5 596 1 US-08-179-738-5 742 4 US-09-107-532A-4996 777 2 US-08-874-678-3 777 4 US-09-348-886-3 1298 1 US-08-340-011-2 1298 1 US-08-340-011-2 1298 3 US-08-901-710-2 1298 4 US-08-901-710-2 1298 5 PCT-USS-042-8-33 1363 1 US-08-874-678-3 1363 2 US-08-874-678-3	ALIGNMENTS	B pplication US/09107532A 75 PATION: 'L LYON: 'L LYON A DOUCELTE-Stamm and David Bush INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES	TEROCOCCUS 310 : THERAPEUTI r Street	STATE: Massachusetts COUNTRY: USA ZIP: 02354 TER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660	107	APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997 ATTORNEY/AGRAT INFORMATION: NAME: Artinello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:	TELEPANE: (781)893-5007  TELEPANE: (781)893-5007  MATION FOR SEQ ID NO: 6348: SEQUENCE TRARACTERISTICS: TYPE: amino acida MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE: ORIGINAL SOURCE: NAME/KEY: misc feature LOCATION: (8) LOCATION 1804 SEQUENCE DESCRIPTION: SEQ ID NO: 6348:
444444444444444444		-532A-6348 e 6348, Applicat No. 6583275 AL INCRMATION: APPLICANT: Lynn TITLE OF INVENTI	NUMBER OF SEQUENCES: 7. CORRESPONDENCE ADDRESS STADDRESSEE: GENOME STREET: 100 Beaver CITY: Waltham	STATE: Massachuse COUNTRY: USA ZIP: 02354 COMPUTER READABLE FORM MEDIUM TYPE: CD/R	COMPUTER: OPERATING SOFTWARE: NT APPLICA APPLICATIC FILING DAT	APPLICATION NUMBER: FILING DATE: 14 May APPLICATION NUMBER: FILING DATE: July 2 NEY/AGENT INFORWATI NAME: Ariniello, Pa REGISTRATION NUMBER REFERENCE/OCCKET NUMBER REFERENCE/OCKET NUMBER REFERENCE/OCKET NUMBER	TELEFAM: (781) 89  MATION FOR SEQ ID NO: SEQUENCE CHARACTEREST  TERESTAGE  TYPE: amino acid  TYPE: amino acid  TYPE: TYPE: protei  HYPOTHETICAL: YES  ORIGINAL SOURCE:  ORGANISM: Entero  FEATURE:  NAME/KEY: misc  LOCATION: (8) 1\overline{10}{10}  SEQUENCE: DESCRIPTON:
28 33 33 33 33 33 33 33 33 34 34 34 34 34 3		1 107 enc nt nt	NUMBE	COMPU	CURREI	ATTORN ATTORN TELECC	INFORMATION FOR SEQ SEQUENCE CHARAC SEQUENCE CHARAC LENGTH: 80 TYPE: amin TYPE: amin TYPE: WOLECULE TYPE: HYPOTHETICAL: Y ORIGINAL SOURCE ORIGINAL SOURCE PEATURE: LOCATION: SEQUENCE DESCRI
	<del></del>	RESULT US-09- ; Sequ		***		** ** ** ** ** ** ** **	H

Db 279 PL-FNLTDLQQEAYRRYKAMGPKETLATLQHLYERHKLVTYPRTDSNYLTDDM 329  Qy 286 QTFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLPPQKATVFHH 330  Db 330 VDTIQERLRAILATDYKSHVRDLISKSFSSKMHIFNNQKVSDHHAIIPTEVR 381  Qy 331LGRYLFHPTNQVWGLVTRY-YEAYLSHADEKIGIQVRVPDE 370  Db 382 PSIEQLSQREFKIYMLIAERFLENLMNPYLYEVLTIHAQLKDYHFVLKEKIPKQL 436  Qy 371 DPQPFQHVMDQISSCTQKEKLLPEVDTLVERSRHVNTPKHKAVLVTSL 418  Cy 371 DPQPFQHVMDGISSCTQKEKLLPEVDTLVERSRHVNTPKHKAVLVTSL 418  Qy 371 DPQPFQHVMDGISSCTQKEKLLPEVDTLVERSRHVNTPKHKAVLVTSL 418  Qy 371 DPQPFQHVMDGISSCTQHTGGGLFKVHRIEIHEHTKAPEYFNEGSLLKAMENPQNH 493  Qy 419HTGGLSKMYWEYPTSTGEIIGVHOPSQEGYQQTEKROMHNGKA 463  Db 494 IDLNDKKYAKTLKHTGGLGTVATRADIIEKLFNNNALESRDGKIKVTSKGKQ 545  Qy 464 LAEMYLLSLTDNLVTSAW-STFGGYVAQGLGGLFFNNNALESRDGKIKVTSKGKQ 545  Qy 464 LAEMYLLSLTDNLVTSAW-STFGGYVAQGLGGLFFNNNALESRDGKIKVTSKGKQ 545  Qy 464 LAEMYLLSLTDNLVTSAW-STFGGYVAQGLGGLFFNNNALESRDGKIKVTSKGKQ 545	Db 546 ILELSPSEL'SPIL'HAQWEEKLANLIERGKYNSQKFİQEMKNFTFKVUNKIKSSEQKYKHD 605  Qy 504 NRTIPD-PSCGRAMSMEPCFHSPPFYDCKAKTGIDTGT 540	# FRIOR FILING DATE: 1998-02-18   PRIOR FILING DATE: 1998-02-18   PRIOR FILING DATE: 1998-07-27   PRIOR FILING DATE: 1998-07-2	137 RNYEKLHKRCGFGTESYKKALKQLDQEHIDGDGECKYVWISFSGLGNRILSLASVFLVA 196	
Query Match   3.7%;   Score   111.5;   DB 4;   Length 804;     Best Local Similarity   21.4%;   Pred. No. 0.019;     Matches   101;   Conservative   61;   Mismatches   132;   Indels   179;   Gaps   26;     Qy	LWLIPGFDDELNKLFPQKATVFHHIGRYLFHPTNQVWGLVTRYYEAYLSHAD 358	Sequence 5060, Application US/09134001C  Sequence 5060, Application US/09134001C  Patent No. 6380370  GENERAL INFORMATION:  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  TITLE OF INVENTION: BPDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  CURRENT APPLICATION NUMBER: US/09/134,001C  CURRENT FILING DATE: 1998-08-13  PRIOR PILING DATE: 1997-11-08  PRIOR PILING DATE: 1997-11-08  PRIOR PILING DATE: 1997-14  NUMBER OF SEQ ID NOS: 5674		113 SRYQSVHYRKPSPYKPSSYLISKLRNYEKLHKRCGPGTESYKKALKQLDQEHID 1

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ORGANISM: Arabidopsis thalians
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Fast
SEQ ID NO 58
LENGTH: 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                147 GPGTESYKKALKQLDQ-----EHIDGDGECKYVVWISFSGLGNRILSLAS 191
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                                                                                                                                                                                                                                                                                                                      Indels 167;
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APPLICANT: Benfey, Philip
APPLICANT: Wysocka-Diller, Joanna
APPLICANT: Wysocka-Diller, Joanna
APPLICANT: Walamy, Jocelyn E.
APPLICANT: Pysh, Leonard
APPLICANT: Pysh, Leonard
APPLICANT: Helariutta, Yrjo
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/186,276B
CURRENT PILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                              Length 993
                                                                                                                                                                                                                                                                            Query Match
3.1%; Score 92.5; DB 4; I
Best Local Similarity 19.1%; Pred. No. 2.7;
Matches 90; Conservative 63; Mismatches 152;
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REPERENCE: 2014/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 993
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PRIOR FILING DATE: 1997-04-24
PRIOR PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 809
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Sequence 58, Application US/09186276B

Patent No. 6388173

GENERAL INFORMATION:
                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Lactococcue sp.
US-08-836-6878-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
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                                                                                                                                                                                                                                                                                  66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
                                                                                                                                                                                                                                                                                                                         63 PPSSNQTLGLANGFYLDDLDFSSLDPPEAYPSQNNNNNNINNKAVAGDLLSSSSDDADFS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 FCEGDQ---TFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 LFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 YAPPPNRLTGKKSHWRDEDEDFVEERSNKOSAVTVEE-SELSEMFDNMFLCGPGKPVC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                   109 DSCLSRYOSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS
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21.7%; Pred. No. 2.2;
ive 52; Mismatches 179; Indels
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APPLICANT: Benfey et al.
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
TITLE OF INVENTION: Thereof.
FILE REFERENCE: 5914-065-99
CURRENT APPLICATION NUMBER: US/08/842,445A
CURRENT FILING DATE: 1997-04-24
BARLIER APPLICATION NUMBER: 08/638,617
BARLIER PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ILNONFPTESAKVVTAQSNG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 VDTLVERSRHVNTPKHKAVLVTSLNAG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    j LOCATION: (1)...(809)
j OTHER INFORMATION: Xaa = Any Amino Acid
US-08-842-445-58
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(809)
CTHER INFORMATION: Xaa = Any Amino Acid
US-09-186-276B-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-842-445-58
; Sequence 58, Application US/08842445A
; Patent No. 6441270
                                                                                                                                                                  Query Match
Best Local Similarity 21.74
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
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LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids FEATURE:
NAME/KEY: SITE
LOCATION: (109)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                      332 YAPPPNRLTGKKSHWRDEDEDFVEERSNKQSÅVYVEE-SELSEMFDNMFLCGPGKPVC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 VEECNGRRAKLLACDGNEIDTMFVDRRGTAEPQGQKLV-----ICCEGNAGFY-EV 290
                                  276 PKKGVEEASKFLPKSSQLFIDVDSY-IP---MNSGSKENGSEVFVKTEKKDETEHHHHHS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 HYRKPSPYK-----PSSYLISKLRNYEKLHKRCGPGT-ESYKKALKQLDQEHIDGDGECK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PCQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 YVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMSWLLPLDFPM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 ITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQGQAR----------- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 PWLIVKTDNYFVPSLWLIPGFDDELNKLPPQKAT------VFHHLGRYLFHPTNQV- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 GCVSTPLEAGYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLG---FQPQDIII 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --W-GLVTRYYEAY--LSH 356
281 FCEGDQ----TFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                 335 LFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 TDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGDQTFIGKV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.0%; Score 91; DB 4; Length 554; Best Local Similarity 19.6%; Pred. No. 1.5; Matches 86; Conservative 50; Mismatches 152; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/489,847

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: PCT/US99/17130

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: 1998-07-30

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 376

SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                        389 -----ILNQNFPTESAKVVTAQSNG 408
                                                                                                                                                                                                        395 VDTLVERSRHVNTPKHKAVLVTSLNAG 421
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 352, Application US/09489847
Patent No. 6476195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (16)
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                                                                                                                                                                                                                                224 WL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMF 280
                                                                                                                                                                                                                                                                   63 PPSSNQTLGLANGFYLDDLDFSSLDPPEAYPSQNNNNNNNNNNNAVAGDLLSSSSDDADFS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSCLSRYQSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI- 165
                                                                          123 DSVLKYISQVLMEEDMEEKPCMFHDALALQAAEKSLYEALGEKDPSSSSASSVDHPERLA 182
                                                                                                                                                                                                                                                                                                                                     281 FCEGDQ---TFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                                                                                                                                                                                                                                                                                  276 PKKGVEBASKFLPKSSQLFIDVDSY-IP---MNGGSKENGSEVFVKTEKKDETEHHHHHS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                       335 LFHPTNOVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 YAPPPNRLTGKKSHWRDEDEDFVEERSNKQSAVYVEE-SELSEMFDNMFLCGPGKPVC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 DSCLSRYQSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 -- DGDGECKYVVWISFSGLGNRILSLASVPLYALLTDRVLLVDRGKDMDDLFCEPFLGMS
                                                                                                                                                                              183 SHSPDGSCS-----GGAFSDYAS-----TTTTTSSDSHWSVDGLENRP---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHSPDGSCS-----GGAFSDYAS-----TTTTTSSDSHWSVDGLENRP---S
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3.1%; Score 92; DB 4; Length 809;
Best Local Similarity 21.7%; Pred. No. 2.2;
Matches 84; Conservative 52; Mismatches 179; Indels
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US-09-186-188B-58

is aguence 58, Application US/09186188B

patent No. 6455672

GENERAL INFORMATION:
TTLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

PILE REFREENCE: 5914-074-999

CURRENT APPLICATION NUMBER: US/09/186,188B

CURRENT FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: 08/842,445

PRIOR APPLICATION NUMBER: 08/842,445

PRIOR APPLICATION NUMBER: 08/638,617

PRIOR FILING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 79

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 VDTLVERSRHVNTPKHKAVLVTSLNAG 421
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LOCATION: (1)...(809)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-186-188B-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Plant
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71 RIMGFAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSCLSRYQSVHYRKPSPYKPS- 129
                                                  ---SKWS---VSNPSPLSRST 168
                                                                                          130 --SYLISKLRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRIL 187
                                                                                                                            169 DLAYIIYT------SGTTGRPKG-------VIVEHHGVNNLQV 198
                                                                                                                                                                                  SLASVFLYALLTDRVLLVDRGKDMD----DLFCEPFLGMSWLLPLDFPMTDQFDGLNQESS 244
                                                                                                                                                                                                                                                                             245 RCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGD------QTFIGKVP 293
                                                                                                                                                                                                                                                                                                            294 WLIVKTDNYFVPSLWLIPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAY 353
                                                                                                                                                                                                                             199 SLSKVFGLRDTDDEVILSFSNYVFDHFVEQMTDAILNGQTLLVLN-----DGMRGDKE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Gutierrez, Santiago
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   311 -------PBRRM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 LSHADEKIGIQVR-----VFDED 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----DKSIGQQVHNSTSYVLNED 354
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                                               132 RİKGMAASGTL---LYPSVLPANPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-222-617A-12
; Sequence 12, Application US/08222617A
; Patent No. 5882879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Veenstra, Annemarie E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 9
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3666 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIKEEL.
CITY: Chicago
STATE: Illinois
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ORIGINAL SOURCE:
ORGANISM: Peni
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APPLICANT:
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                                                                            460 EEGLRVVRQWLEASSQLEEASIYSRWEVEEDWCLSVLRSYQAEHGPDFPWSVGEDMSADG 519
348 YAWSIGGFTATWAAMSYPDVSAMILDASFDDLVPLALKVMPDSWRGLVTRTVRQHLNLNN 407
                                          357 ADEKIGIQVRVFDEDPGP---FQHVMDQISSCTQKEKLLPB--VDTLVERSRH----VNT 407
                                                                                                                                       -----YPTSTGEIIGVHQ 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Garcia, Bruno D.
APPLICANT: Garcia, Bruno D.
APPLICANT: Barredo, Jose L.
APPLICANT: Barredo, Jose L.
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Autibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/note= "Domain II of ACV Synthetase from
Penicillium chrysogenum; aa 1397-2154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.0%; Score 90; DB 2; Length 758;
Best Local Similarity 20.7%; Pred. No. 3.2;
Matches 67; Conservative 35; Mismatches 99; Indels 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Proppy disk
COMPUTER: Parent PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
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                                                                                                                                408 PKHKAVLVTSLNAGYAENLKSMY--WE
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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520 RRQLALFLARKHLHNFEA 537
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ATTORNEY AGENT INPORMATION:
REFERENCE/DOCKET NUMBER: 9
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
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FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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OTHER INFORMATION:
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LOCATION: 1..758
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1648 KLYRYIEKNRVTYLSGTPSVVSMYBFSRFKDHLRRVDCVGEAFSEPVFDKIRETFHGLV- 1706
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Antibiotic Production and for Isolation of Large
Quantities of ACV Synthetase
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CURRENT APPLICATION DATA:
PLEICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
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                                                                                                                                                                                 3.0%; Score 90;
20.7%; Pred. No.
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Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
Van Liempt, Henk
Montenegro, Eduardo P.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Martin, Juan F.
Garcia, Bruno D.
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
LENGTH: 3727 amino acids
                                                                                                                                                                                    Query Match
Best Local Similarity 20.7*
Matches 67; Conservative
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                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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STREET: SUC
CITY: Chicago
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US-08-222-617A-27
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APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                        Gaps
                                                             /label= region
/note= "Region of ACV Synthetase; aa 62-3727"
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                                                                                                                                                                                       Score 90; DB 2; Length 3666;
Pred. No. 43;
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APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
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Patent No. 5882879
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 27:
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Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
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Garcia, Bruno D.
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Best Local Similarity 20.7%
Matches 67; Conservative
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                                COCATION: 1..3666
COTHER INFORMATION:
COTHER INFORMATION:
US-08-222-617A-12
      NAME/KEY: Protein
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US-08-222-617A-27
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                                                                                                                                                                  843 DGIINQRAFYNYLSAWATNDVFAYGASQGKL--YPEPRQYFHQPNEYDLKIPKSLPLVYA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QESSRCYGYM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 VKNQVIDTEGTLSH-LYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 SMYAV--TQGNFEYPTQQQLLRDY--HDSF------RVPH-VIKNDNGGLPDFWL 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 IPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 EDPGPFQHVMDQISSCTQKEKLLPEVDT-----LVERSRHVNTPKHKAVLVTS--LNA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791 E------EYRDGRLTKECWFPNASSDAILAYKLIVQTGHVDNPVDKELVLTNRLVNS 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SEWLGNLOKIFD 790
                                                                                                                    421 GYAENLKSMY------WEYPTSTGELIGVHQPSQEGYQQTEKKMHNGKAL----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SCOTT, MATHEW P
APPLICANT: GCODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 PFLGMSW-----LLPLDFPMTDQFDGLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Flehr, Hohbach, Test, Albritton
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.0%; Score 89; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   776 L-----LP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 6, Application US/08540406; Patent No. 5837538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: a601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
NFORMATION FOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.03
Best Local Similarity 20.33
Matches 63, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      EM--YLLSLTD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-540-406-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    1528 RİKGMAASGTL---LYPSVLPANPD------SKWS---VSNPSPLSRST 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VTVEHHGVVNLQV 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1595 ŚLSKVFGLRDTDDEVILSFSNYVFDHFVEQMTDAILNGQTLLVLN------DGMRGDKE 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...--INGYGPTEVSITTHKRLYPF-PERRM------ 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 --SYLISKLRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRIL 187
                                                                                                                                                                                                                                                                                                                                    71 RIMGFAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSCLSRYQSVHYRKPSFYKPS- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 SLASVFLYALLTDRVLLVDRGKDMD---DLFCEPFLGMSWLLPLDFPMTDQFDGLNQESS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QTFIGKVP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 WLIVKTDNYFVPSLWLIPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT Genmill, Robert M.
APPLICANT: Genmill, Harry A.
TITLE DEAbkin, Harry A.
FILLE REFERENCE: 93445-0004
CURRENT APPLICATION NUMBER: US/09/268,140
CURRENT APPLICATION NUMBER: US/09/268,140
PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR PLICATION NUMBER: US 60/077,723
PRIOR FILLING DATE: 1998-03-12
SOFTWARE: PACHILL VOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 PFLGMSW-------QESSRCYGYM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672 PFLMRSWVKFLTVMGFLAALISSLYASTRLODGLDIIDLVPKDSNEHKFLDAQTRLFGFY 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 VKNQVIDTEGTLSH-LYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 IPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFD 369
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                                                                                                                                                                                                                                                                                   Gарв
                                                                                                                                                                                                                                                                               99; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Indels 125;
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                                                                                                                                                                                                            DB 2; Length 3778;
45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 RCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1565 DLAYIİYT-----SGİTGRPKG----
                                                                                                                                                                                                  Query Match
3.0%; Score 90; DB 2
Best Local Similarity 20.7%; Pred. No. 45;
Matches 67; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%; Score 89.5; DF
20.6%; Pred. No. 8.7;
tive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DKSIGQQVHNSTSYVLNED 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 LSHADEKIGIQVR-----VFDED 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09268140 Patent No. 6268176 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 1286
; TYPE: PRT
TYPE: PRT
OSGANISM: Drosophila melanogaster
US-09-268-140-3
       3778 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 20.6
Matches 64; Conservative
                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                ; MODECULE IXE
US-08-222-617A-2
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-268-140-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 777
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Query Match 3.0%; Score 89; DB 3; Length 1285;
Best Local Similarity 20.3%; Pred. No. 9.8;
Matches 63; Conservative 39; Mismatches 83; Indels 126; Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 GYAENLKSMY-------WEYPTSTGEIIGVHQPSQEGYQQTEKKMHNGKAL----A 465
                           251 VKNQVIDTEGTLSH-LYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 IPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 L-----SEWLGNLOKIFD 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LVERSRHVNTPKHKAVLVTS--LNA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 PPLGMSW-----QESSRCYGYM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672 PFLMRSWVKFLTVMGFLAALISSLYASTRLQDGLDIIDLVPKDSNEHKFLDAQTRLFGFY 731
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                        RESULT 15
US-08-656-055-6
Sequence 6, Application US/08656055
Patent No. 6027882
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOORICH, LISA V
APPLICANT: GOORICH, LISA V
APPLICANT: GOORICH, LISA V
APPLICANT: GONENCE, 19
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIF: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 EDPGPFQHVMDQISSCTQKEKLLPEVDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REERERNEE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
                                                                                466 EM--YLLSLTD 474
:| || || 900 QMPFYLHGLTD 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-055-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Four Embarca
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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        QY
        421 GYAENLKSMY--------WEYPTSTGEIIGVHQPSQEGYQQTEKKWHNGKAL----A 465

        Db
        842 DGIINQRAFYNYLSAWATNDVFAYGASQGKL--YPEPRQYFHQPNEYDLKIPKSLPLVYA 899

        QY
        466 EM--YLLSLTD 474

        Db
        900 QMPFYLHGLTD 910

        Search completed: January 30, 2004, 15:36:22

        JOb time: 22 secs
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791 E-----EYRDGRLTKECWFPNASSDAILAYKLIVQTGHVDNPVDKELVLTNRLVNS 841

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Sequence 152, App
Sequence 612, App
Sequence 815, App
Sequence 304, App
Sequence 303, App
Sequence 303, App
Sequence 304, App
Sequence 22315, A
Sequence 58, Appl
Sequence 58, Appl
Sequence 68, Appl
Sequence 646, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, Appli
6, Appli
                                                                                                                ; Search time 39 Seconds
(without alignments)
2973.483 Million cell updates/sec
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Sequence 152, A
Sequence 612, A
Sequence 835, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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                                                                                                                                                                                        US-10-037-311B-1
3004
1 MDQNSYRRRSSPIRTTTGGS.....GTLVPHVRHCEDISWGLKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-259-194A-152
US-09-882-227-612
US-10-238-075-835
US-10-032-2018-305
US-10-032-2018-305
US-10-032-2018-304
US-10-369-493-19663
US-10-369-493-19663
US-10-369-493-1947
US-10-369-493-19347
US-09-849-905A-6
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               789580 seqs, 207824079 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                              January 30, 2004, 15:34:17
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                     Scoring table:
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994.5
103.5
103.5
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                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                              Run on:
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16 90.5 3.0 419 15 US-10-197-666A-134 Sequence 134, App Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 13660, A Sequence 1
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## ALIGNMEN

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Associated with Growth in Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 FPNV--TNINSDKLLGGLLASGFDEDSCLSRYQSVH-YRKPSPYKPSSYLISKLRNYEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 HKRCGPGTESYKKALKQLDQEHI-DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Sequence 35. Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: United States Department of Agriculture
; APPLICANT: Howen, Benjamin A
; APPLICANT: Buckler, Edward S
; TITLE OF INVENTION: Identification of Genes Associated
; FILE REFERENCE: 37-00510US
; CURRENT APPLICATION NUMBER: US/10/338,777
; CURRENT PILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARR: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
49.7%; Score 1492; DB 12;
Best Local Similarity 54.6%; Pred. No. 7.6e-147;
Matches 295; Conservative 90; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 533
TYPE: RRT
; ORGANISM: Arabidopsis thaliana
US-10-338-777-35
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 35
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264 296

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APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 612
LENGTH: 658
412 ---TGKPPPDNDNDDLATAYDS--NSSNGSGGGNYSALLIASLYPDYYERIRATYYEHA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| || : ||: ||| 527 RPIILMPAHGHRVPAPPCRRAVSMEPCNLTPPRVGEAECREMAAVVDKEDVARHVKVCED 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 LLGGLLASGFDEDSCLSRYQSVHYRKPSPYKPSSYLISKLRNYEKLHKRCGPGTESYKKA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---MIVWISLDKGKDDPQLIFESMNSKDIELTQT----DLIRNYIVME 175
                                                                                                                                                                                                        KATVFHHLGRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQ-HVMDQI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 LKQLDQEHIDGDGECKYVVWIS-----FSGLGNRILSLASVFLYALLTDRVLLV 205
                                                                                                                                                                                                                                                                               383 SSCTQK-----EKLLPEVDTLVERSRHVNTPKHKAVLVTSLNAGYAENLKSMYWEYP 434
                                                                                                                                                                                                                                                                                                                                                        435 TSTGEIIGVHQPSQEGYQQTEKKMHNGKALAEMYLLSLTDNLVTSAWSTFGYVAQGLGGL 494
                                                                                           238 PPGATWILPPDFPVANLF-GLGPRPEQSYTTILNKKKITAVVNNDDDPASKNATAALPPP
                                                                                                                                -LYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLFPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                495 KPWILYRPENRTTPDPSCGRAMSMEPCFHSPPFY---DCKAKTG-IDTGTLVPHVRHCED
                                                                                                                                                                                                                                                                                                                                                                             37 GTMKLIRIFITCLIVFSVLVAFSMIFHQHPSDSNRIMGFAEARVLDAGVFPNVTNINSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 12; Length 658; 0.064;
                                                           219 FLGMSWLLPLDFPMTDQFDGLNQESSRCYGYMVKNQVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.064; 79; Mismatches 191;
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17.8%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 612, Application US/09882227
Publication No. US20030158396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 17.8
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 ISWGLK 556
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                      178
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                                                                                                 230 SIPPHLYMHNLHDSRDSDKLFVCQKDQSLIDKVPWLIVQANVYFVPSLWFNPTFQTELVK 289
                                                                                                                                                                        DQVISCTQREKLLPEFATPESKYNISKTPKLKSVLVASLYPEFSGNLTNMFSKRPSSTG 409
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   VLLVDRGKUMDDLFCEPFLGMSWLLPLDFPMTDQFD--GLNQESSRCYGYMVKNQVIDTE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLDQEHIDGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLIVESVLVAFSMIFHOHPSDSNRIM------GFAEARVLDAGVFPNVTNINSDKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moughamer, Todd
Provart, Nicholas
Ricke, Darrell
Zhu, Tong
FENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IDEA

TITLE OF INVENTION: IDEA

FILE REFERENCE: 70029-NP

CURRENT APPLICATION NUMBER: US/10/259,194A

CURRENT FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR PLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-04

PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04

SEQ ID NOS: 662

SOFTWARE: PatentList.pl Version 3.0.4 (C) 2001 Syngenta
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40.8%; Pred. No. 1.2e-94;
Live 76; Mismatches 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 152, Application US/10259194A; Publication No. US20040010815A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glazebrook, Jane
Goff, Stephen A.
Katagiri, Fumiyaki
Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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Best Local S
Matches 223
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APPLICANT:
APPLICANT:
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APPLICANT: Vicinity Canaly
APPLICANT: Redulide, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reduler, Lynne
APPLICANT: Rechman, Jose Luis
APPLICANT: Riechman, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
ITILE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REPRENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT APPLICATION NUMBER: 60/227439
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR PILING DATE: 2000-08-22
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 516
SSOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3%; Score 99; DB 11; Length 76 Best Local Similarity 21.8%; Pred. No. 1.2; Matches 85; Conservative 54; Mismatches 173; Indels
          Sequence 504, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Arabidopsis thaliana US-09-934-455-504
                                                                 APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-10-032-201B-305
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TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: B.coli, and biological uses of these polynucleotides and of their FILE REFERENCE: BLANDINE CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT APPLICATION NUMBER: 0003145

PRIOR PILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: Patentin version 3.1
                                     176 TEVEKQEDFYNQYWRAMEERFEQNETLFNRFVRHYLTIKIGKIPNEKRVYEAFKDYRQKK 235
                                                                                                                                                            277 DKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGF-----DDELNKLFP---- 322
                                                                                                                                                                                     323 --OKATVFHHLGRYLF-----HPTNOVWGLV-----TRYYEAYLSHADEKIG 362
                                                                                                                                                                                                                                                                                                                      363 IQVRVFDEDPGPFQHVMDQISSCTQXEKLLPEVDTLVERSRHV--NTPKHKAVLVTSLNA 420
                                                                                                               236 GIEIEDLLKDLGKYCGYPCQIAPKKEDDKDLNKALSFLVNLEMDVIYPLLLELYSDYKD- 294
                                                                                                                                                                                                                                                                       336 HIQKDEYFKSLKAHFVCLTEKQRPPNNDEFKKLFITIDFYKFKKNKYFLERLENFDTKEP 395
                                                                                                                                                                                                                                                                                                                                                 396 V----DTQKCNIEHIMPQTLTPEWQRDLGENFQAIHEKYLHTIGN-----LTLTGYNS 444
                                                                                                                                                                                                                                                                                                                                                                                                              -----YWEYPTST 437
                                                                                                                                                                                                                                                                                                                                                                                                                                            445 KYSNNSFQEKRDMEKGFKOSSLKLNQSLKDLESFGEKRIEKRASDLADWALKIWTYPILE 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 EKLLPE----VDTLVERSRHVNTPK------HKAVLVTSLNAG--YAENLKSMYWEYP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||:|
253 TIYGEIVGFATNCDAAHITQPQRETMQYCMEQSLKIAGLSAQDIGYISAHGTATDRGDMA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 TSTGEIIG------VHQPSQEGYQQTEKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 ----DGLNQESSRCYGYMV-----KNQVIDTEGTLSH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 GEIIGVHQPSQEGYQQTEKKMHNGKALAEMYLLS 471
                                                                                                                                                                                                                                                                                                                                                                                                        206 DRGKDMDDLFCEPFLGMSWLLPLDFPMTDQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 835, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
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ORGANISM: Escherichia coli
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Matches 53;
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66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
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                                                                                                                                                                                                                                                 84 DSVLKYISQVLMEEDMEEKPCMFHDALALQAAEKSLYEALG---EKYPSSSSASSVDHPE 140
                                                                                                                                                                                                                                                                                                                                  -----GDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFL 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AMQFKKGVEBASKFLPKSSQLFIDVDSY-IP---MNSGSKENGSEVFVKTEKKDETEHHH 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 GMSWL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHD 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 GRYLFHPTNOVWGLVTRYYEAYLSHADEKIGIOVRVFDEDPGPFQHVMDQISSCTQKEKL 391
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                                                                                                                    24 PPSSNQTLGLANGFYLDDLDFSSLDPPEAYPSQNNNNNNINNKAVAGDLLSSSSDDADFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 RLASDSPDGSCS-----GGAFSDYAS-----TTTTTSSDSHWSVDGLENRP--
78;
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RESULT

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APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
TITLE OF INVENTION: MAURICE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 3814 35.B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 528
TYPE- ----
TYPE- ----
                                                                                                                                                                                                                                                                                                                                                                                                            285 KKL---PTNQL-----QVTWEDHASGK------EDTGTFDTVLWAIGR----- 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 GRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKL 391
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                                                                                                                                                                                                      282 CEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLFPQ------KATVFHHL 331
                                                                                                                                                                                                                                                                     233 CAGFLÍGIGLDTTVMMRS----IP----LRGFDQQMSSLVTEHMESHGTQFLKGCVPSHI 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 YQQTEKKMHNGKALAE-MYLLSLT----DNLVTSAWSTFGYVAQGLGGLKPWIL--
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                                                                   Length 524;
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                                                               3.2%; Score 96; DB 12;
21.2%; Pred. No. 1.3;
iive 40; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YRPENRTTPDPSCGRAMSMEPCFHSPP 526
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3.2%; Score 96; DB 1
Best Local Similarity 21.2%; Pred. No. 1.3;
Matches 58; Conservative 40; Mismatches
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319 VPETRTLNLEKAGISTNPKNQKIIVDAQEA---
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LOCATION: S27
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-032-201B-304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-10-032-201B-304
; Sequence 304, Application US/10032201B
; Publication No. US20030167524A1
                                                                                               Best Local Similarity 21.2
Matches 58; Conservative
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JS-10-032-201B-303
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                                                                      Query Match
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                                                                             APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Steed
APPLICANT: Dalmia, Steve
APPLICANT: Zaplachinski, Steve
APPLICANT: Maloney, Mautic, Steve
APPLICANT: Moloney, Mautic, Steve
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
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APPLICANT: Heiferz, Peter Bernard
APPLICANT: Heiferz, Peter Bernard
APPLICANT: Heiferz, Peter Bernard
APPLICANT: Briggs, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Steve
APPLICANT: Zaplachinski, Steve
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION WINNER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
WUMBER OF SEQ ID NOS: 313
SOFTWARE: FRASEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 EVYHAYYKPLEFTVADRDASOCYIKMVCMREPP 453
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LOCATION: 523
OTHER INFORMATION: Xaa = Any Amino Acid
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                                   Peter Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Van Rooijen, Gijs
                                                                   Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
US-10-032-201B-305
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ORGANISM: Mus musculus
                               Heifetz,
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IN PLANTS FOR PRODUCTION

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Query Match
3.1%; Score 93; DB 12; Length 1418;
Best Local Similarity 19.3%; Pred. No. 13;
Matches 110; Conservative 86; Mismatches 208; Indels 166;
                                            APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DONSYRRSSPIRTTGGSKSVNFSELLOMKYLSSGTMKL
                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Saccharomyces cerevisiae US-10-369-493-22315
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US-10-253-007-58
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APPLICANT: Cao, Yongwei
APPLICANT: Starer, Steven C.
APPLICANT: Starer, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS MITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052) WITH IMPROVED PROPERTIES
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US (6)360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                           428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 LFCEPFLGMSWLLPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDY 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 RLFHGRG----GTVGRGGGPSYQGILAQPPGSVSGQIRLTEQGEVIASKYTDPEIGRRNLE 678
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451 YQQTEKKMHNGKALAE-MYLLSLT----DNLVTSAWSTFGYVAQGLGGLKPWIL-----
                          369 PELTPTAIKAGKLLAQRIFGKSSTLMDYSNVPTTVFTPLEYGCVGLSEERAVALHGQEHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 LRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVWI------SFS---
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1 Similarity 19.5%; Pred. No. 3.3;
81; Conservative 68; Mismatches 146; Indels 120;
                                                                                                   EVYHAYYKPLEFTVADRDASQCYIKMVCMREPP 461
                                                                       ----YRPENRTTPDPSCGRAMSMEPCFHSPP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
: LOCATION: (1)..(934)
: OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-19663
                                                                                                                                                                                             Sequence 19663, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 81, Conserva
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LENGTH: 934
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                                                                                                                                                                                                                                                                                                                          137 RNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRILSLASVFLYA 196
                                                                                                                                                                                                                                                                                                                                                                               276 ES-------SYTEVTKLLKNBGIDLDHK-----RFLILOGEVENIAQMKPKA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                       197 LLTDRVLLVDRGKDMDD----LFCEPFLGMSWLLPLPLDFPWTDQFDGLNQESSRCYGYMVKN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 QVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 BIVDREKNSL-----ESGKETALEFLEKEK--------------------------- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---RSKLPQFK-----LLQSNSKLASTLEKISSSNKDLEDEKMKFQESLKKVDEI 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 GYAEN----LKSMYWEYPTSTGEIIGVHQPSQEGYQQTEKKWHNGKALAEMYLLSLTDNL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHKSYSQ--SPPRSP--GRSPTRRLELLQLSPVKNSRVELQKIYDRHQSSSKQQSRLFIN
                                                                                                 48 CLIV--FSVLVAFSMIFHOHPSDSNRI--MGFAEARVLDAGVFPNVTNINSDKLLGGLLA
                                                                                                                                     ----TRTFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benfey et al. TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 58, Application US/10253007; Publication No. US20030088073A1; GENERAL INFORMATION:
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US-10-369-493-22315 ; Sequence 22315, Application US/10369493

371

Length 946;

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376 AETLNLSGL--KGYTTGGTV------HVVINNQVGFTTDPHDSRSSLYSTAIA 420
                                                                                                                                                                                                                                                                                                                         79 RVLDAGVFPNVTNINSD-----KLLGGLLASGFDED----SCLSRYQSVHYRKPS 124
                                                                                                                                                                                                                                                                                                                                                                    421 OMLDIPVF----HVNGDDPEACVHIAKLVAEYROT-FKSDVVIDLVCYRRYGHNEGDEPS 475
                                                                                                                                                                                                                                                                                                                                                                                                                 125 PYKPSSYLI-----SKLRNYEKLHKRCGPGTESYKKALKOLDQEHID-----G 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DMDDLFCEPFLGM-----SWLLPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTE-GTL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVERTVIKKRLGMLDSGELQW-----SEGESLAYATLLSEGYNIRITGQDCERGTF 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHLYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLFP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 QKATVFHHLGRYLFH----PTNQVWGLVTRYYBAYLSHADEKIGIQVRVFDEDPGPFQHV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 MDQ-ISSCTQKEKLLPEVDTLVERSRHVNTPKH-KAVLVTSLNAGYAENLKSMYWEYPTS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 IDOFIAAGESKWRRLSGLTLLLPHGYEGOGPEHSSARLERFLDLCAEDNIOVC---YPTT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :: | | : | | : | | 529 RQESQFKEPSALEGLWKPYQGGALKSADV---STAVDKQVLCDALRKLSTLPEGFNVHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 SKSVNFSELLOMKYLSSGTMKLTRTTTCLIVFSVLVAFSMIFHQHPSDS-NRIMGFAEA
                                                                                                                                   Query Match 3.1%; Score 92; DB 12; Lengtn 940; Best Local Similarity 21.7%; Pred. No. 8.9; Matches 105; Conservative 63; Mismatches 166; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 DGECKYVVWISFSGL----GNRILSLASVFLYALLTDRVLLVDR--
                                           TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                          US-10-369-493-19347
SEQ ID NO 19347
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Starts S.
APPLICANT: Gredory J.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
FILE TILE OF DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US (6)369,493
CURRENT APPLICATION NUMBER: US (6)360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPSSNQTLGLANGFYLDDLDFSSLDPPEAYPSQNNNNNNINNKAVAGDLLSSSSDDADFS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 WLHTPMPSNF----VFQSTSRSNSVTGGGGGGNSAVYGSGFGDDLVSNMFKD----VBLAMQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVLKYISQVLMEEDMEEKPCMFHDALALQAAEKSLYEALGEKDPSSSSASSVDHPERLA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 SHSPDGSCS-----GGAPSDYAS-----TTTTTSSDSHWSVDGLENRP----S 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCEGDQ----TPIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 LFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; Score 92; DB 15; Length 809;
21.7%; Pred. No. 6.9;
ive 52; Mismatches 179; Indels
                FILE REFERENCE: 5914-074-999
CURRENT APPLICATION NUMBER: US/10/253,007
CURRENT TLING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: US/09/186,188
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR APPLICATION NUMBER: 08/638,617
PRIOR APPLICATION NUMBER: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 VDTLVERSRHVNTPKHKAVLVTSLNAG 421
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-253-007-58
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Publication No. US20030233675A1
GENERAL INFORMATION:
Thereof
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Matches 84; Conservative
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plant
                                                                                                                                                                                                                                                                              SEQ ID NO 58
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                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DANDER: 10s/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 91; DB 1
Pred. No. 4.4;
Sequence 646, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Deinococcus radiodurans
US-10-369-493-646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.0%;
19.8%;
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Db 155 PAAGFDSSKNIFLGEKAAKWK NPDGHMDGLTTN 187  Qy 357 ADEXIGIQVR	RESULT 15 US-10-317-250-6 ; Sequence 6, Application US/10317250 ; Sequence 6, Application No. US20030165945A1 ; GENERAL INFORMATION: ; APPLICANT: Bird, Timothy A. ; APPLICANT: Li, Xiaoxia ; APPLICANT: Li, Xiaoxia ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES ; CURRENT APPLICATION NUMBER: US/10/317,250 ; CURRENT FILING DATE: 2002-12-11 ; NUMBER OF SEQ ID NOS: 15 ; SOFTWARE: Patentin version 3:1 ; SEQ ID NO 6 ; LENGTH: 419 ; TYPE: PRT ; ORGANISM: Mus musculus US-10-317-250-6	Matches 61; Dength 419; Beet Local Similarity 19.2%; Pred. No. 3.4; Matches 61; Conservative 42; Mismatches 96; Indels 119; Gaps 61; Conservative 42; Mismatches 96; Indels 119; Gaps 178 SFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMD-DLFCEPFLGMSWLLPLPFPMTDOF 1		Search completed: January 30, 2004, 15:40:58 Job time : 40 secs
Matches         100;         Conservative         43;         Mismatches         177;         Indels         184;         Gaps         20;           QY         54         VLVAPEMIFHQHPSDRNRIMGFAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSC         111	263 290 304 347 405 465 465	RESULT 14 US-09-843-905A-6 is Sequence 6, Application US/09843905A is Patent No. US20020168683A1 is Patent No. US20020168683A1 is Patent No. US20020168683A1 is PAPLICANT: Bird, Timothy A. is APPLICANT: Comman, David J. is TITLE OF INVENION: HUMAN PELLINO POLYPEPTIDES is FILE REFERENCE: 2990-A is CURRENT PILING DATE: 2001-04-27 is CURRENT FILING DATE: 2000-04-28 is NUMBER OF SEQ ID NOS: 15 is SOFTWARE: Patentin version 3.1 is SEQ ID NO 6 is LENTH: 419 is TYPE: PRT	) ARCANISM: Mus musculus US-09-843-905A-6 US-09-843-905A-6 Query Match Best Local Similarity 19.2%; Pred. No. 3.4; Matches 61; Conservative 42; Mismatches 96; Indels 119; Gaps 16;	OY 178 SPSGLGNRILSLASVELYALLTDRVLLVDRGKDMD-DLFCEPFLGMSWLLPLDFPWTDQF 236  1

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